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RAW SEQUENCE LISTING

DATE: 02/19/2002

PATENT APPLICATION: US/10/021,368

TIME: 11:52:38

Input Set : N:\Crf3\RULE60\10021368.txt
 Output Set: N:\CRF3\02192002\J021368.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Band, Vimla
 8 (ii) TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
 9 MOLECULES AND METHODS
 11 (iii) NUMBER OF SEQUENCES: 11
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: Fish & Richardson P.C.
 15 (B) STREET: 225 Franklin Street
 16 (C) CITY: Boston
 17 (D) STATE: MA
 18 (E) COUNTRY: USA
 19 (F) ZIP: 02110-2804
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/10/021,368
 C--> 29 (B) FILING DATE: 12-Dec-2001
 34 (C) CLASSIFICATION:
 31 (vii) PRIOR APPLICATION DATA:
 32 (A) APPLICATION NUMBER: 09/201,038
 33 (B) FILING DATE:
 36 (viii) ATTORNEY/AGENT INFORMATION:
 37 (A) NAME: Clark, Paul T.
 38 (B) REGISTRATION NUMBER: 30,162
 39 (C) REFERENCE/LOCKET NUMBER: 00398/100002
 41 (ix) TELECOMMUNICATION INFORMATION:
 42 (A) TELEPHONE: 617/542-5070
 43 (B) TELEFAX: 617/542-8906
 44 (C) TELEX: 200154
 47 (2) INFORMATION FOR SEQ ID NO: 1:
 49 (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 276 amino acids
 51 (B) TYPE: amino acid
 52 (C) STRANDEDNESS: not relevant
 53 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 62 Met Arg Ala Pro His Leu His Leu Ser Ala Ala Ser Gly Ala Arg Ala
 63 1 5 10 15

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65   Leu Ala Lys Leu Leu Pro Leu Leu Met Ala Gln Leu Trp Ala Ala Glu
66           20                25                30
69   Ala Ala Leu Leu Pro Gln Asn Asp Thr Arg Leu Asp Pro Glu Ala Tyr
70           35                40                45
72   Gly Ala Pro Cys Ala Arg Gly Ser Gln Pro Trp Gln Val Ser Leu Phe
73           50                55                60
75   Asn Gly Leu Ser Phe His Cys Ala Gly Val Leu Val Asp Gln Ser Trp
76           65                70                75                80
78   Val Leu Thr Ala Ala His Cys Gly Asn Lys Pro Leu Trp Ala Arg Val
79           85                90                95
81   Gly Asp Asp His Leu Leu Leu Leu Gln Gly Glu Gln Leu Arg Arg Thr
82           100               105               110
84   Thr Arg Ser Val Val His Pro Lys Tyr His Gln Gly Ser Gly Pro Ile
85           115               120               125
87   Leu Pro Arg Arg Thr Asp Glu His Asp Leu Met Leu Leu Lys Leu Ala
88           130               135               140
90   Arg Pro Val Val Pro Gly Pro Arg Val Arg Ala Leu Gln Leu Pro Tyr
91           145               150               155               160
93   Arg Cys Ala Gln Pro Gly Asp Gln Cys Gln Val Ala Gly Trp Gly Thr
94           165               170               175
96   Thr Ala Ala Arg Arg Val Lys Tyr Asn Lys Gly Leu Thr Cys Ser Ser
97           180               185               190
99   Ile Thr Ile Leu Ser Pro Lys Glu Cys Glu Val Phe Tyr Pro Gly Val
100          195               200               205
102   Val Thr Asn Asn Met Ile Cys Ala Gly Leu Asp Arg Gly Gln Asp Pro
103          210               215               220
105   Cys Gln Ser Asp Ser Gly Gly Pro Leu Val Cys Asp Glu Thr Leu Gln
106          225               230               235               240
108   Gly Ile Leu Ser Trp Gly Val Tyr Pro Cys Gly Ser Ala Gln His Pro
109          245               250               255
111   Ala Val Tyr Thr Gln Ile Cys Lys Tyr Met Ser Trp Ile Asn Lys Val
112          260               265               270
114   Ile Arg Ser Asn
115          275
117 (2) INFORMATION FOR SEQ ID NO: 2:
119     (i) SEQUENCE CHARACTERISTICS:
120         (A) LENGTH: 1454 base pairs
121         (B) TYPE: nucleic acid
122         (C) STRANDEDNESS: single
123         (D) TOPOLOGY: linear
125     (ii) MOLECULE TYPE: cDNA
130     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
132 ACCAGCGGCA GACCACAGGC AGGGCAGAGG CACGTCTGGG TCCCCTCCCT CCTTCCTATC      60
134 GGCAGACTCCC AGATCCTGGC CATGAGAGCT CCGCACCTCC ACCTCTCCGC CGCCTCTGGC      120
136 GCCCGGGCTC TGGCGAAGCT GCTGCCGCTG CTGATGGCGC AACTCTGGGC CGCAGAGGCG      180
138 GCGCTGCTCC CCCAAAACGA CACGCGCTTG GACCCCGAAG CCTATGGCGC CCGGTGCGCG      240
140 CGCGGCTCGC AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT      300
142 GTCCTGGTGG ACCAGAGTTG GGTGCTGACG GCCGCGCACT GCGGAAACAA GCCACTGTGG      360
144 GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAGGGCG AGCAGCTCCG CCGGACGACT      420

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146 CGCTCTGTTG TCCATCCCAA GTACCACCAG GGCTCAGGCC CCATCCTGCC AAGGCGAACG      480
148 GATGAGCACG ATCTCATGTT GCTAAAGCTG GCCAGGCCCG TAGTGCCGGG GCCCCGCGTC      540
150 CGGGCCCTGC AGCTTCCTTA CCGCTGTGCT CAGCCCGGAG ACCAGTGCCA GGTGTGCTGGC      600
152 TGGGGCACCA CGGCCGCCCC GAGAGTGAAG TACAACAAGG GCCTGACCTG CTCCAGCATC      660
154 ACTATCCTGA GCCCTAAAGA GTGTGAGGTC TTCTACCCCTG GCGTGGTCAC CAACAACATG      720
156 ATATGTGCTG GACTGGACCG GGGCCAGGAC CCTTGCCAGA GTGACTCTGG AGGCCCCCTG      780
158 GTCTGTGACG AGACCCTCCA AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC      840
160 CAGCATCCAG CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA      900
162 CGCTCCAACG GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT CCTGCTGATC      960
164 CAGATGCCCA GAGGCTCCAT CGTCCAFCCCT CTTCCTCCCC AGTCGGCTGA ACTCTCCCCCT    1020
166 TGTCTGCACT GTTCAAACTT CTGCGCGCCT CCACACCTCT AAACATCTCC CCTCTCACTT    1080
168 CATTCCCCCA CCTATCCCCA TTCTCTGCCCT GTACTGAAGC TGAAATGCAG GAAGTGGTGG    1140
170 CAAAGGTTTA TTCCAGAGAA GCCAGGAAGC CGGTCAATCAG CCAGCCCTCT AGAGCAGTTA    1200
172 CTGGGGTTCAC CCAACCTGAC TTCTCTGCCCT ACTCCCCGCT GTGTGACTTI GGGCAAGCCA    1260
174 AGTGCCCTCT CTGAACCTCA GTTTCCTCAT CTGCAAAATG GGAACAATGA CGTGCCCTACC    1320
176 TCITAGACAT GTTGIGAGGA GACTATGATA TAACATGTGT ATGTAAATCT TCATGTGATF    1380
178 GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTTCTGACT AAAGGTTACC TGTGTGCTG      1440
180 AAAAAAAAAA AAAA                                1454

```

182 (2) INFORMATION FOR SEQ ID NO: 3:

184 (i) SEQUENCE CHARACTERISTICS:

185 (A) LENGTH: 19 base pairs

186 (B) TYPE: nucleic acid

187 (C) STRANDEDNESS: single

188 (D) TOPOLOGY: linear

190 (ii) MOLECULE TYPE: cDNA

195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

197 CCGCAGATTT AGGTGACAC

19

199 (2) INFORMATION FOR SEQ ID NO: 4:

201 (i) SEQUENCE CHARACTERISTICS:

202 (A) LENGTH: 19 base pairs

203 (B) TYPE: nucleic acid

204 (C) STRANDEDNESS: single

205 (D) TOPOLOGY: linear

207 (ii) MOLECULE TYPE: cDNA

212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

214 GGCCTCTAAT ACGACTCAC

19

216 (2) INFORMATION FOR SEQ ID NO: 5:

218 (i) SEQUENCE CHARACTERISTICS:

219 (A) LENGTH: 17 base pairs

220 (B) TYPE: nucleic acid

221 (C) STRANDEDNESS: single

222 (D) TOPOLOGY: linear

224 (ii) MOLECULE TYPE: cDNA

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

231 TACCACTACA ATGGATG

17

233 (2) INFORMATION FOR SEQ ID NO: 6:

235 (i) SEQUENCE CHARACTERISTICS:

236 (A) LENGTH: 20 base pairs

237 (B) TYPE: nucleic acid

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238 (C) STRANDEDNESS: single
 239 (D) TOPOLOGY: linear
 241 (ii) MOLECULE TYPE: cDNA
 246 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 248 GTTGAAGTGA ACTTGCGGGC 20
 250 (2) INFORMATION FOR SEQ ID NO: 7:
 252 (i) SEQUENCE CHARACTERISTICS:
 253 (A) LENGTH: 281 amino acids
 254 (B) TYPE: amino acid
 255 (C) STRANDEDNESS: not relevant
 256 (D) TOPOLOGY: linear
 258 (ii) MOLECULE TYPE: protein
 263 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 265 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Phe
 266 1 5 10 15
 268 Pro Val Asp Asp Asp Lys Ile Val Gly Gly Tyr Met Met Thr Arg
 269 20 25 30
 271 Tyr Ala Arg Thr Cys Arg Glu Ser Ser Val Pro Tyr Gln Val Ser Leu
 272 35 40 45
 274 Asn Ala Gly Tyr His Phe Cys Gly Gly Ser Leu Ile Asn Asp Gln Trp
 275 50 55 60
 277 Val Val Ser Ala Ala His Cys Tyr Lys Tyr Arg Ile Gln Val Arg Leu
 278 65 70 75 80
 280 Gly Glu His Asn Met Met Thr Arg Tyr Ala Arg Ile Asn Val Leu Glu
 281 85 90 95
 283 Gly Asn Glu Gln Phe Val Asp Ser Ala Lys Ile Ile Arg His Pro Asn
 284 100 105 110
 286 Tyr Asn Ser Trp Thr Leu Asp Asn Asp Ile Met Leu Ile Lys Leu Ala
 287 115 120 125
 289 Ser Pro Val Thr Leu Met Met Thr Arg Tyr Ala Arg Asn Ala Arg Val
 290 130 135 140
 292 Ala Ser Val Pro Leu Pro Ser Ser Cys Ala Pro Ala Gly Thr Gln Cys
 293 145 150 155 160
 295 Leu Ile Ser Gly Trp Gly Asn Thr Leu Ser Asn Gly Val Asn Asn Pro
 296 165 170 175
 298 Asp Leu Leu Gln Cys Val Asp Ala Pro Val Leu Pro Gln Ala Met Met
 299 180 185 190
 301 Thr Arg Tyr Ala Arg Asp Cys Glu Ala Ser Tyr Pro Gly Asp Ile Thr
 302 195 200 205
 304 Asn Asn Met Ile Cys Val Gly Phe Leu Glu Gly Gly Lys Asp Ser Cys
 305 210 215 220
 307 Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Glu Leu Gln Gly
 308 225 230 235 240
 310 Ile Val Ser Trp Gly Tyr Met Met Thr Arg Tyr Ala Arg Gly Cys Ala
 311 245 250 255
 313 Gln Pro Asp Ala Pro Gly Val Tyr Thr Lys Val Cys Asn Tyr Val Asp
 314 260 265 270
 316 Trp Ile Gln Asn Thr Ile Ala Asp Asn
 317 275 280

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Input Set : N:\Crif3\RULE60\10021368.txt

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319 (2) INFORMATION FOR SEQ ID NO: 8:

321 (i) SEQUENCE CHARACTERISTICS:

322 (A) LENGTH: 299 amino acids

323 (B) TYPE: amino acid

324 (C) STRANDEDNESS: not relevant

325 (D) TOPOLOGY: linear

327 (ii) MOLECULE TYPE: protein

332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

334 Leu Glu Leu His Pro Leu Leu Gly Gly Arg Thr Trp Arg Ala Ala Arg
335      1          5          10          15
337 Asp Ala Asp Gly Cys Glu Ala Leu Gly Thr Val Ala Val Pro Phe Asp
338      20          25          30
340 Asp Asp Asp Lys Ile Val Gly Gly Tyr His Ser Thr Arg Tyr Ile Val
341      35          40          45
343 Asx Thr Cys Glu Asn Ser Leu Pro Tyr Gln Val Ser Leu Asn Ser Gly
344      50          55          60
346 Ser His Phe Cys Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser
347      65          70          75          80
349 Ala Ala His Cys Tyr Lys Thr Arg Ile Gln Val Arg Leu Gly Glu His
350      85          90          95
352 Asn His Ser Thr Arg Tyr Ile Val Asx Ile Lys Val Leu Glu Gly Asn
353      100         105         110
355 Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His Pro Lys Tyr Asn
356      115         120         125
358 Arg Asp Thr Leu Asp Asn Asp Ile Met Leu Ile Lys Leu Ser Ser Pro
359      130         135         140
361 Ala Val Ile His Ser Thr Arg Tyr Ile Val Asx Asn Ala Arg Val Ser
362      145         150         155         160
364 Thr Ile Ser Leu Pro Thr Ala Pro Pro Ala Ala Gly Thr Glu Cys Leu
365      165         170         175
367 Ile Ser Gly Trp Gly Asn Thr Leu Ser Phe Gly Ala Asp Tyr Pro Asp
368      180         185         190
370 Glu Leu Lys Cys Leu Asp Ala Pro Val Leu Thr Gln Ala His Ser Thr
371      195         200         205
373 Arg Tyr Ile Val Asx Glu Cys Lys Ala Ser Tyr Pro Gly Lys Ile Thr
374      210         215         220
376 Asn Ser Met Phe Cys Val Gly Phe Leu Glu Gly Gly Lys Asp Ser Cys
377      225         230         235         240
379 Gln Arg Asp Ser Gly Gly Pro Val Val Cys Asn Gly Gln Leu Gln Gly
380      245         250         255
382 Val Val Ser Trp Gly His His Ser Thr Arg Tyr Ile Val Asx Gly Cys
383      260         265         270
385 Ala Trp Lys Asn Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val
386      275         280         285
388 Asp Trp Ile Lys Asp Thr Ile Ala Ala Asn Ser
389      290         295

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391 (2) INFORMATION FOR SEQ ID NO: 9:

393 (i) SEQUENCE CHARACTERISTICS:

394 (A) LENGTH: 286 amino acids

VERIFICATION SUMMARY

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TIME: 11:52:39

Input Set : N:\Crf3\RULE60\10021368.txt

Output Set: N:\CRF3\02192002\J021368.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]